BLAST 2 SEQUENCES
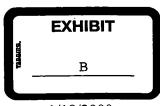
This tool produces the alignment of two given sequences using <u>BLAST</u> engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program [blastp ▼] Matrix [0 BLOSUM62 ▼]

Parameters used in <u>BLASTN</u> program only:

Reward for a match: [＿＿＿] **Penalty for a mismatch:** [＿＿＿]

Open gap [11] and extension gap [1] penalties

gap x_dropoff [50] expect [1000] word size [2] Filter ☐

Sequence 1 Enter accession or GI [＿＿＿＿]

or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
YTSALQP
```

Light chain CDR2

Murine 21.6

Sequence 2 Enter accession or GI [＿＿＿＿]

or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
GISNRFS
```

residues 75-81 of
SEQ ID NO: 12

[Align] [Clear Input]

Comments and suggetstions to: <u>blast-help@ncbi.nlm.nih.gov</u>
Credits to: <u>Tatiana Tatusov</u> and <u>Tom Madden</u>

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix `0 BLOSUM62` gap open: `11` gap extension: `1`
x_dropoff: `50` expect: `1000` wordsize: `2` Filter ☐ `Align`

Sequence 1 lcl|seq_1 **Length** 7
Sequence 2 lcl|seq_2 **Length** 7
No siginificant similarity was found